

FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG
ACCATCCTGGGTGCGTGGCTGAACCTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATAACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACC
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCCAGCTGCAGGGACAGACCCCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCCGGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAGTCCAGGTTGCCCGCCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

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FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRITYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQ RATANMLATMSNPLGVLVANVLSPVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQ LQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAATGMIFVLGQAE GILIMLMTALT VRRSEPSLSTCQQGEDPLDWT VSLLLMAGLCTFF
SCILAVFFHTPYRRLQAESGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAA TDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

Important features:**Potential Transmembrane domains:**

amino acids 30-50, 61-79, 98-112, 126-146, 169-182, 201-215, 248-268, 280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

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FIGURE 170A

GTCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTCCATCATTTGCT
GAAGTGGACCAACTAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGG
ACATCTCAGATCGCTTCCAATGAAGATGGCCTTGCCTTGGGGTCTGCTTGTTCATAATCA
TCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGGAAGGAGCACGGGGCTGATCAAGC
CATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGTCTTCTGAATCTA
GCCCCTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGG
TGGCTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAG
TGTGAGAGGAAGTGCCATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAACTGGGGCCGGAG
GAGAGGCGGAGGCAAGCTGGGGCCGCCTTCCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCAT
TCAGGTGGACTCTGAGGAAGGCTTGTCTAGCACAGGCAGGCGGCTGGATCGAGAGCAGCTGT
GCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTTGGCTCTG
ATCCATGTGGAGATCCAAGTGCTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGA
GCAGGAGCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACC CGGATCCCCCTGGACAGAGCTC
TTGACCCAGACACAGGCCCTAACACCCTGCACACCTACACTCTGTCTCCAGTGAGCACTTT
GCCTTGGATGTCAATTGTGGGCCCTGATGAGACCAAACATGCAGAACTCATAGTGGTGAAGGA
CCTGGACAGGGAAATCCATTCAATTTTTTGATCTGGTGTTAACTGCCTATGACAATGGGAACC
CCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGCTTGGACTCCAATGACAATAGCCCT
GCGTTTGCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCT
CATAAAATGACCGCCACAGACCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCTCA
GTAAGCACATGCCTCCAGAGGTGCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTC
ATTCTGCGTCGACCTCTAGACTATGAAAAGAACCCTGCCTACGAGGTGGATGTTTCAGGCAAG
GGACCTGGGTCCCAATCCTATCCCAGCCATTGCAAAGTTCTCATCAAGGTTCTGGATGTCA
ATGACAACATCCCAAGCATCCACGTACATGGGCCTCCCAGCCATCACTGGTGTGAGAAGCT
CTTCCCAAGGACAGTTTTATTTGCTCTTGTGTCATGGCAGATGACTTGGATTGAGGACACAATGG
TTTGGTCCACTGCTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCA
ACACATACATGTTGCTAACCAATGCCACACTGGACAGAGAGCAGTGGCCCCAAATATACCCCTC
ACTCTGTTAGCCCAAGACCAAGGACTCCAGCCCTTATCAGCCAAGAAACAGCTCAGCATTC
GATCAGTGACATCAACGACAATGCACCTGTGTTGAGAAAAGCAGGTATGAAGTCTCCACGC
GGGAAAACAACCTTACCCTCTCTTCACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGC
ATTAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGA
CTCCAACACAGGAGAGGTCAGTCTGCTCAGAGGTCACTGAACTATGAAGAGATGGCCGGCTTTG
AGTTCCAGGTGATCGCAGAGGACAGCGGGCAACCCATGCTTGCATCCAGTGTCTCTGTGTGG
GTCAGCCTCTTGGATGCCAATGATAATGCCCCAGAGGTGGTCCAGCCTGTGCTCAGCGATGG
AAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCCCATCGAGA
CTCCCAATGGCTTGGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGG
CCATTCTTTTTGACAACCATTTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCT
CTACAGCATCCGCAATGGAAATGAAGCCACCTCTTCATCCTCAACCCTCATACGGGGCAGC
TGTTTCGTCAATGTCACCAATGCCAGCAGCCTCATTGGGAGTGAGTGGGAGCTGGAGATAGTA
GTAGAGGACCAGGGAAGCCCCCCTTACAGACCCGAGCCCTGTTGAGGGTCATGTTTGTCAC
CAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGATGCTGA
CGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTGATCCTGGCTTTGTTTCATGTCC
ATCTGCCGGACAGAAAAGAAGGACAACAGGGCCTACAACCTGTCGGGAGGCCGAGTCCACCTA
CCGCCAGCAGCCCAAGAGGCCCCAGAAACACATTCAGAAGGCAGACATCCACCTCGTGCCTG
TGCTCAGGGGTCAGGCAGGTGAGCCTTGTGAAGTCGGGCAGTCCCACAAAGATGTGGACAAG
GAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTTCCACCTACCCCGAC
CCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACCGGCGGAGAGCCGAGAGGTGC
TGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAGAGGAATGCCTCCCGGGAGAAC
CTGAACCTTCCCGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCTCTGAAGGTTGC
AGGCAGCCCCACAGGGAGGCTGGCTGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCAC
CAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCTCAATGGCAAAGTGTCCCTTGAGAAA
GAATCAGGGCCCCGTGAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGCTGCCTTCGCCGA
GCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTAGCAAATCTCCAGCTGC
TGTCTTGCTGCATCAGGGCCAATTCCAGCCCCAAACCAACCCAGGGAATAAGTACTTG
GCCAAGCCAGGAGGCAGCAGGAGTGCAATCCCAGACACAGATGGCCCAAGTGCAAGGGCTGG

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FIGURE 170B

AGGCCAGACAGACCCAGAACAGGAGGAAGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGA
AGCAACTGCTAGAGAAGAGCTGTCAAGTCTGCTGGACCCCAGCACAGGTCTGGCCCTGGAC
CGGCTGAGCGCCCCCTGACCCGGCCTGGATGGCGAGACTCTCTTTGCCCTCACCACCAACTA
CCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGT
TCGGCAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTC
TCGGAGATGAGCTCACTGCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCCTGGAGGC
CGCCTCCGAGGCGCTGCGGCGGCTCTCGGTCTGCGGGAGGACCCTCAGTTTAGACTTGGCCA
CCAGTGACAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGGAAAGACGGGGACTGAGGGC
AAGAGCAGAGGCAGCAGCAGCAGCAGCAGGTGCCTGTGAACATACCTCAGACGCCTCTGGAT
CCAAGAACCAGGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACCTCAC
TAGCTAGCGGCGGCCTGAGAACTTTAGGGTGAAGTATGCTACCCCCACAGAGGAGGCAAGAG
CCCCAGGACTAACAGCTGACTGACCAAAGCAGCCCCTTGTAAGCAGCTCTGAGTCTTTTGGG
GGACAGGGACGGTTTGTGGCTGAGATAAGTGTTTCCTGGCAAAACATATGTGGAGCACAAAG
GGTCAGTCCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGGAAAGGGTGGCCTTCTT
GGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTATCAA
TAAAGGAAAAGCAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSNDNSPAFAESS
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQRSLNVEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDDA
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTT
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQQPKRPQKHIOKADIHLVPVLRGQAGEPCEVGQSHKDVVDKEAMMEA
GWDPCQLQAPFHLTPTLYRTLNRQGNQGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEPGGS
RSAIPD TDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEEELSSLLDPSTGLALDRLSAPD
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDPPGGKTGTEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTTCTCAGCCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGAATCTC
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATAACACTTACATGTCTTACTTCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAACAAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCATAACTCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTGAGGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTTAAGGTTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAGGGCGGCCGCGACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFEMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAIS
SKSSNVIVLLLAQIMGMVFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:**Signal peptide:**

amino acids 1-23

Potential transmembrane domains:amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

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FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTTGGATTTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTNNNGNATACCTTCCCAGAAAATATTTTTTGGATTGTTGGGTAGNTT
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN
TAGGAGATCCCTTTCCCATTCTC

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FIGURE 176A

CTCGCGCAGGGATCGTCCC**ATGG**CCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGA
TTTGCTACCTTTTTTGGCTCCCTGCTCGTCAACTGCTCTTCTCACGGGCTGTGCCTTCAAT
CTGGACGTGATGGGTGCCTTGCAGCAAGGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGT
GGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTGGCTGCTGGTGGGTGCTCCCCAGG
CCCTGGCTCTTCTTGGGAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTGCCCGTTGAGC
CTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAG
CAAGGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCCTGGGGGCAAGATTGTTA
CCTGTGCACACCGATATGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATG
ATTGGTCGCTGCTTTGTGCTCAGCCAGGACCTGGCCATCCGGGATGAGTTGGATGGTGGGGA
ATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATTTGGGTTCTGCCAGCAGGGCA
CAGCTGCCGCCTTCTCCCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAACCTATAAT
TGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGA
CGACGGTCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCCTCATCCCGGTCCCTG
CCAACAGCTACTTTGGCTTCTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTG
AGCTTTGTGGCTGGAGCCCCCGCGCCAACCACAAGGGTCTGTGTGTCATCCTGCGCAAGGA
CAGCGCCAGTCGCCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCGCCTGACCTCCGGCTTTG
GCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGGTGCC
CCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGG
GGGTCACTGGGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCCTGACTCCATGTTTCGGGA
TCAGCCTGGCTGTCCTGGGGGACCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCC
CCCTTTGATGGTGTGGGAAAGTCTTCATCTACCATGGGAGCAGCCTGGGGGTGTGCGCAA
ACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGGCTACTCCCTGTCAG
GCAGTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACACC
GCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACG
AAGCATCGACCTGGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGG
TCTGTTTCAGCTACATTGCAGTCCCCAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTG
TTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGTTCCCCGTGTGACGTTCCCTGAGCCG
TAACCTGGAAGAACCCAAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCACCAGCATGACC
GAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATT
GTAGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGG
GCTGCCTCCAGTGGCCCCCATCCTCAATGCCCACCAGCCCAGCACCCAGCGGGCAGAGATCC
ACTTCTGAAGCAAGGCTGTGGTGAAGACAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAC
GCCCCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACCTCTGCCCATGGATGTGGATGG
AACAACAGCCCTGTTTGCAGTGTGGGAGGAGTCAATTGGCCTGGAGCTGATGGTACCA
ACCTGCCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCATGAAGCCCAGCTC
CTGGTCATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAA
GCCACTCTGCCTGTCCAATGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGA
AGAGAGGTGCCAGGTACCTTCTACCTCATCCTTAGCACCTCCGGGATCAGCATTGAGACC
ACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCAGGAGCTGCATCCAGTCTC
TGCACGAGCCCGTGTCTTCAATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCCCCAGC
AACTCTTCTTCTGCTGTTGGTGGTGGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGC
AGCAAGGTCAAGTATGAGGTACCGGTTTCCAACCAAGGCCAGTCGCTCAGAACCCTGGGCTC
TGCCTTCTCAACATCATGTGGCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAA
TGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCTGGGCAGAAAGGGCTTTGCTCTCCAGGCCC
AACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGCGGGAGCTGGAGCCACCTGA
GCAGCAGAGCCTGGTGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGCTG
AGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACCTGTGTGGTGTTCAGC
TGCCCACTCTACAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAG
CACCTTTCTGGAGGAGTACTCAGCTGTGAAGTCCCTGGAAGTGATTGTCCGGGGCCAACATCA
CAGTGAAGTCCCTCCATAAAGAACTTGATGCTCCGAGATGCCTCCACAGTGATCCAGTGATG
GTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCCTGGTGGGTGATCCTCCTGGC
TGTACTGGCTGGGCTGCTGGTGTGCTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCT
TCAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGG
GAAGACCGACAGCAGTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAG

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FIGURE 176B

CCCCGGCGGGAGGGCCCGGATGCACACCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGG
GCCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCCCATGTCCCAGCCTGGCCTGTGG
CTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGTGGGCTGCTG
GTGTCGCATCAAGATTTGGCAGGATCGGCTTCCTCAGGGGCACAGACCTCTCCCACCCACAA
GAACTCCTCCCACCCAACCTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGAC
AGGGCCATGGGGTAGGGTGAGAAGGGCAGGGGTGTCCTGATGCAAAGGTGGGGAGAAGGGAT
CCTAATCCCTTCCTCTCCCATTCACCCTGTGTAAACAGGACCCCAAGGACCTGCCTCCCCGGA
AGTGCCTTAACCTAGAGGGTCGGGGAGGAGGTTGTGTCACTGACTCAGGCTGCTCCTTCTCT
AGTTTCCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGTTTCGTC
TATTTATTAAAAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAAA

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGWKFCEG
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEEELGGAVYVYLNQGGHWAGI
SPLRLCGSPDSMFGISLAVLGDNLQDGFDPDIAVGAPFDGDGKVFYIYHGSSLGVVAKPSQVLE
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSLSLQTPRLRRQAPGQGLPPVAP
ILNAHQ PSTQRAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPOADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSN
ENASHVECELGNPMKRG AQVT FYLILSTSGIS IETTELEV ELLLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKEYEVTVSNOGQSLRTLGS AFLNIM
WPHEIANGKWL LYPMQVELEGGQGPQKGLCSRPNIHLHDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWVPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDR AAVLHVWGR LWNSTFLEEY
SAVKSLEVIVRANITVKSSIKNMLLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVLAGLL
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGS PRREGP
DAHPILAADGHPELGPDPGHPGPETA

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 1039-1064

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTGCGACGGCGGTAATTTTC
TGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTTCGATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAACAGACTTGATACAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAATTATTTGAAAATTCAGCTAAAGTTATAGAAGTTTATGTTTAAAT
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAGAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTACGAGAACAACTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTTGAAAG
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAA

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FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPCLMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTKTLRPERSRFDTSILPI
CKDSLGMFMNRLDTNYDLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDLSLNNEWCYCFQ
RQQDPPECQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDRYGNEVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

Important features:**Signal peptide:**

amino acids 1-16

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

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FIGURE 180A

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAA
CAGTACCTGACGCCTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGC
TGCCCTTCCCCGTGCTCCTTCTGGCCGCTCTGCCTCCGGTGCTGCTGCCTGGGGCGGCCGGC
TTCACACCTTCCCTCGATAGCGACTTCACCTTTACCTTCCC GCCGCCGAGAAAGGAGTGCTT
CTACCAGCCCATGCCCCCTGAAGGCCTCGCTGGAGATCGAGTACCAAGTTTTAGATGGAGCAG
GATTAGATATTGATTTCCATCTTGCCCTCTCCAGAAGGCCAAAACCTTAGTTTTTGAACAAAGA
AAATCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAA
TACATTCAGCACCATTCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAG
AACAGGCACAAGAACAAGAAGATTGGAAGAAATATATTACTGGCACAGATATATTGGATATG
AAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCCAGACTAAGCAAAAGTGGGCA
CATACAAATTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGCAACTTTG
ATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTTCATGGTGGTGGTGTCAGCCATTCAA
GTTTATATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAACT
AGAGTACGTAACATTGAAAAATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCAT
TAATGGTCTTCTCCAAAATATTTTGGAGATATAAAAGTAGGAAACAGGTATAATTTTAATGTG
AAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAGTTGTACTTAAGTGTGTA
ACAGGAATATTTTGCAGAAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCATTTTC
CTAACTTTGAAAAATTTTGCAAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAAT
TGCAACACCAGTCTGTTTTTAACAGGTTCTATTACCCAGAACTTTTTTGTAAATGCGGCAGT
TACAAATTAAGTGTGGAAGTTTTTCAGTTTTTAAGTTATAAATCACCTGAGAATTACCTAATGA
TGGATTGAATAAATCTTTAGACTACAAAAGCCCACTTTTCTCTATTTACATATGCATCTCT
CCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTGGAGTTTTTATAACC
AAATACATTTTCAGTGTAAATATATTAGCAGAAAGCATTAGTCTTTGTACTTTGCTTACATTCC
CAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACAT
GTTTTCTCTTTGAAATGAAGAATATAGTTTTAAAGCTTCCTCCTCCATAGGGACACATTTTC
TCTAACCCTTAACTAAAGTGTAGGATTTTAAATTAATGTGAGGTAAAATAAGTTTTATTTT
TAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAATAATCATGTTATGTTAATTTTAAC
ATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATATTGCTAAAATG
ATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGG
AAAGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAATTCACTTAAGTAGAACTAT
AAATAAATATCTAGAATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGG
AGATGATTAATTTCCAGTTAGCTGGAAGAACTTTGGCTGTAGGTTTTTATTTTCTACAAGA
ATTCTGGTTTGAATTATTTTGTAAAGCAGGTACATTTTATAAAATGTAAGCCCTACTGTAAG
GTTTAGCACTGGGTGTACATATTTATTAAAAATTTTATTATAACAACTTTTATTAAAAATGG
CCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTT
TTAAACACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGA
AGTCTATGGGGGTCTTACTCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAATTT
TTAAGTTATGCCCATTTATAACGTTGTTTATGACTACATTGTGAGTTAGAAACAACTTAA
ATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATTCCTGATGAGCAATAATGA
TAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCCTCTTA
GGCCCTTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTTTAAAAATGAGGTAA
TGCCGTATATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGCTTAGGGGTATCC
TCTGCAACACTTGCAGAACAAGGTCAATAAGATCCTTGCCATGAATACCCCTCCCTTTTG
CGCTGTTAAATTTGCAATGAGAAGCAAATTTACAGTACCATAACTAATAAAGCAGGGTACAG
ATATAAACTACTGCATCTTTCTATAAAACTGTGATTAAGAATTCACCTCTCCTGTATGGC
TGTTACTGTACTGTACTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCTAC
ATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAAAC
GATAATTGCTTTATTTGGAAAAGAAATTTAGGAATACTAAGGACAATTATTTTTTATAGACAAA
GTAAAAAGACAGATATTTAAGAGGCATAACCAAAAAAGCAAACTTGTAACAGAGTAAAAA
TCTTTAATATTTCTAAAGACATACTGTTTATCTGCTTCATATGCTTTTTTTTAAATTTCACTAT
TCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTTAACAGCTCATTT
TGTCTTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTT
CCATAATGTAGCAGTTACCGTGTTACCTCACACTAAGGCCTAGAGTTTGCTCTGATATGCA
TTTGGATGATTAATGTTATGCTGTTCTTTTCATGTGAATGTCAAGACATGGAGGGTGTGTTGTA

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FIGURE 180B

ATTTTATGGTAAAATTAATCCTTCTTACACATAATGGTGTCTTAAAATTGACAAAAATGAG
CACTTACAATTGTATGTCTCCTCAAATGAAGATTCTTTATGTGAAATTTTAAAAGACATTGA
TTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTTGCTCAAACG
CTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATA
ATAAAAATTATCAAAGGAAAA

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FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEY
QVLGDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFTEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

Important features:**Signal peptide:**

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

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FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGAT
CTCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCCAGTGTGTCCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT
TTTTGTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC
TTCTTTTTCCTTTTTCTTCACCTTCATTTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 183

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM
DADLACQKRPSGKLVSVLGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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FIGURE 184

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCAATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP
FQGDSTVTKSCASKCKPSDVDGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

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FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG
TAGCGGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA
GACACTAAACCAGCTATCCAAATGCAGTGAACCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

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FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQTIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGOVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

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FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

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FIGURE 189A

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATC
CCGTGCGCCGCGGCTGGGCCGTCGGAGAGTGCCTTCTCTCTGACGCGGTGCTTGG
GCTCGGCCAGGCGGGGTCCGCCGCCAGGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGAC
CCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGAAGTATTAGAAATGAGCTGAAGAC
CATTCACAGATTAATATTTTTGGGGACAGATTTGTGATGCTTGATTACCCCTTGAAGTAATG
TAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTT
CACTTAAATCAGAACTTGCATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATA
TCAGAGACTTGAAAAGGATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGC
ACAGATCAGGATTTTTACAGTTTACTTGGAGTGTCCAAACTGCAAGCAGTAGAGAAATAAG
ACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAAAAACCCGAATAACCCAAATG
CACATGGCGATTTTTTAAAAATAATAGAGCATATGAAGTACTCAAAGATGAAGATCTACGG
AAAAAGTATGACAAATATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAG
CTGGAACATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGG
AAAGAAGAGAATTTGATGCTGCTGTTAATTCTGGAGAAGTGTGGTTTGTAATTTTTACTCC
CCAGGCTGTTTACACTGCCATGATTTAGCTCCACATGGAGAGACTTTGCTAAAGAAGTGGA
TGGGTACTTTCGAATTGGAGCTGTTAAGTGTGGTGATGATAGAATGCTTTGCCGAATGAAAG
GAGTCAACAGCTATCCAGTCTCTTCATTTTTTCGGTCTGGAATGGCCCCAGTGAAATATCAT
GGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTCGCAATGCAGCATGTTAGAAGTACAGTGAC
AGAACTTTGGACAGGAAATTTTGTCAACTCCATACAAACTGCTTTTGCTGCTGGTATTGGCT
GGCTGATCACTTTTTTGTTCAAAAGGAGGAGATTGTTTGACTTCACAGACGACTCAGGCTT
AGTGGCATGTTGTTTTCTCAACTCATTGGATGCTAAAGAAATATATTTGGAAGTAATACATAA
TCTTCCAGATTTTGAAGTACTTTTCGGCAAACACACTAGAGGATCGTTTGCTCATCATCGGT
GGCTGTTATTTTTTTCATTTTGGAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAACTA
AAAACCTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGACTGTTCTCTGCACCGA
CATCTGTAGTAATCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCA
AAGAATATGAAATTCATCATGGAAAGAAGATTCTATATGATATACTTGCCCTTTGCCAAAGAA
AGTGTGAATTCTCATGTTACCACGCTTGGACCTCAAATTTTTCTGCCAATGACAAAGAACC
ATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACTACCAGAGTTAC
GAAGAGCATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCAT
GAGGGACTCTGTAACATGTATAACATTCAAGGCTTATCCAACAACAGTGGTATTCAACCAGTC
CAACATTCATGAGTATGAAGGACATCACTCTGCTGAACAAATCTTGAGGTTTCATAGAGGATC
TTATGAATCCTTCAGTGGTCTCCCTTACACCCACCACCTTCAACGAAGTATTACACAAAGA
AAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTGGTGTGTCATCCTTGCCAAGTCTT
AATGCCAGAATGGAAAAGAATGGCCCGGACATTAAGTGGACTGATCAACGTGGGCAGTATAG
ATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGA
TTTTTTCCCCCAAATCAAATAAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGA
TGCTTATTCCCTGAGAATCTGGGGTCTAGGATTTTTTACCTCAAGTATCCACAGATCTAACAC
CTCAGACTTTTCAGTGAAAAGTTCTACAAGGGGAAAATCATTGGGTGATTGATTTCTATGCT
CCTTGGTGTGGACCTTGCCAGAATTTTGCTCCAGAATTTGAGCTCTTGGCTAGGATGATTAA
AGGAAAAGTGAAAGCTGGAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAAAGCTG
GGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAA
GAAGAGCAGATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAAATTTGGA
AACTCTCCGAAATCAAGGCAAGAGGAATAAGGATGAACTTTGATAATGTTGAAGATGAAGAA
AAAGTTTAAAAGAAATTTGACAGATGACATCAGAAGACACCTATTTAGAATGTTACATTTA
TGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCAGAATTATCTACAGCA
CTGGTGTAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTAGA
CTTTGCAGGCTATAATATATGGTTCACACATGAGAACAAGAATAGAGTCATCATGTATTCTT
TGTTATTTGCTTTTAAACAACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACA
AAAGTAGGCTGGATTTCAGTCCATGGACCATAGATTGCTGTCCCCCTCGACGGACTTATAATG
TTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCTATCTACATAAATGTCTAAGTTGTAT
AAAGTCCACTTTCCCTTCACGTTTTTTGGCTGACCTGAAAAGAGGTAAGTTAGTTTTTGGTC
ACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTTCGTTTTTAAACACCCA
TGATGTGGCACAGTAAACAAACCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTT
TTCTTTCTTCTCAAAGGTTGAAAAATGCTTTTTAATTTTTTACAGCCGAGAAACAGTGCAG

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FIGURE 189B

CAGTATATGTGCACACAGTAAGTACACAAATTTGAGCAACAGTAAGTGCACAAATTCTGTAG
TTTGCTGTATCATCCAGGAAAACCTGAGGGAAAAAAATTATAGCAATTAAGTGGGCATTGTA
GAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATATGTGTTTAT
GTATTTTCTGAAATTGCTTTCATAGAAATTTTCCCACTGATAGTTGATTTTGTAGGCATCTA
ATATTTACATATTTGCCTTCTGAACCTTTGTTTTGACCTGTATCCTTTATTTACATTGGGTTT
TTCTTTCATAGTTTTTGGTTTTTCACTCCTGTCCAGTCTATTTATTATTCAAATAGGAAAAAT
TACTTTACAGGTTGTTTTTACTGTAGCTTATAATGATACTGTAGTTATTCAGTTACTAGTTT
ACTGTCAGAGGGCTGCCTTTTTTCAGATAAATATTGACATAATAACTGAAGTTATTTTTATAA
GAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTAGACTCAA
GAATCACAAATTTGTCAGTAACATGTAGTTGTTTAGTTATAATTCAGAGTGTACAGAATGGT
AAAAATCCAATCAGTCAAAAGAGGTCAATGAATTAAAAGGCTTGCAACTTTTTCAAAAAA
AAAAA

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FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL
HPDKNPNNPNAHGDFLKINRAYEVLKDEDLRKKYDKYGEKGLLEDNQGGQYESWNYRYDFGI
YDDDPEIITLERREFDAAVNSGELWVFNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS
IQTAFAAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN
TLEDRLAHRWLLFFHFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP
SLAVFKGQGTKEYEIHGKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS
AEQILEFIEDLMNPSVVS LTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG
FLPQVSTDLTPTQTFSEKVLQGNHWVIDFYAPWCGPCQNFAPFEFELLARMIKGKVKAGKVDC
QAYAQTQCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

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FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGA
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCCAGTTTTTGTGAATACTGGGTTCACCA
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA
GATGGAATACTTACCAATAAGAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTGAG
ACTACAGAAGTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTTGAATCAATGCTGCAAAGCTTTATTTTCACATTTTT
TCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA
ATTACCTGTCTTCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCTCTT
TCATGCCTCTTAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAGATTGAGCATTGAAAGATTTCCCTAGCCTCTTCTCTTT
TCATTAGCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCTCCCTTTTTATAGTCTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA
TAACCTTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

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FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAAECKRLGVTAHAYVVDSCNREEIYRSLNQVKKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRSLID
GILTNNKKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCCAGCCCGCCGGGGC
AGGATGACCAAGGCCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT
GCTGATCATCGTGTAAGTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGACACAGTCCTTCT
CTAGGCCGCACACGGGGCCGCGCTGCCACGCCCCGGGCCGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGACACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG
CAAGTTCGCCGTGCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTGAAGCTTTCGCGTTGCTTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

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FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGVSVMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELT
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFTKERAFFDDIPNSELHSLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLHHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELENEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFLFGYPKPENLLRD

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

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FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATTT
CTACTTGGGGCCCCCTTCCTAGGACTCTCCCACCCCAAACCTCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTGCAGCC

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FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNNAGHHPPQORPEETSAQGFRQLLELNLLGTYTLTKL
ALPYLRKSQGNVINISSLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTGG
AELGYGCKASRSTPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

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FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACTG
CTGTTTCTTCTTACCATTTCCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCTGGCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTACGGATGAAACCGTATGCCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCG
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSRIPVDLPEARCLCL
GCVNPFTMQEDRSMVSVFVSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

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FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGGTGGGCGCTGCGGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT
TACGCCCCATGGTGTCCATCCTGCCAGCAGACTGATTCAAGAATGGGAGGCTTTTGCAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG
GCCGCTTCTTTGTCACCACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT
TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACCTATTTACAGTGACTCTTGGAATT
CCTGCTTGGTGTCTTATGTGTTTTTCGTCATAGCCACCTTGGTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAAGTGAGGCCAATGATCAGGGGGCCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC
TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC
TGTAGATTTAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCTGAATGAGCAAGCTTCTCTTAAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT
GACAAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGGAGACTGGGATGGGAA
CAAGTTCATTTACTTAGGGGTGAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGATCCTTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTACAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTTT
AAGTTTTCTAAGCAATATTTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTCCCTGGGTCTTGAAC
TACTTTAATAATAACTAAAAAACCACTTCTGATTTTCTTTCAGTGATGTGCTTTTGGTGAAA
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG
GCTAATTTCTTT

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMASNWTLMEGEWMLKIFYAP
WCPSCQQTDSEWEAFAKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSEERSEQNRRSEEAHRAEQLODAEEEEK
DDSNEEENKDSLVDDEEEKEDLGDEDEAEEDNLAAGVDEERSEANDQGPPGEDGVTRE
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSHADKGL

Important features:**Signal peptide:**

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

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FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAV
VLGTMGVLSSPCPPNWIIYEKSCYLEFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Important features:**Type II transmembrane domain:**

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

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FIGURE 203A

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCCAGACCTGGAGGG
TCTCGCTCTGTACACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACC
TCCCGGGTTCAAGTGATTCTCATGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGAC
TTCCAAGAGTGACTCCGTCGGAGGAAAATGACTCCCCAGTCGCTGCTGCAGACGACACTGTT
CCTGCTGAGTCTGCTCTTCCCTGGTCCAAGGTGCCACGGCAGGGGCCACAGGGAAGACTTTC
GCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGAC
CTGCGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCCCTTTCCTGCGAGC
CCACCCTGCTTCCCGATCCTTCCCTGACCCAGGGGCCTCTACCACTTCTGCCTCTACTGGA
ACCGACATGCTGGGAGATTACATCTTCTCTATGGCAAGCGTGACTTCTTGCTGAGTGACAAA
GCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTGGCTCAGGGCCCCCGCTGTT
AGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCCGCCAGCT
TCACCTTCTCCTTCCACAGTCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGC
GAGCTCAAAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATCCCCAGAAGGCCTCAAG
GAGGCCCTCGGCTGCCCCCGCCAGCCAGCAGTTGCAGAGCCTGGAGTCGAAACTGACCTCTG
TGAGATTCAATGGGGGACATGGTGTCTTTCGAGGAGGACCGGATCAACGCCACGGTGTGGAAG
CTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGGCAGGAGGAGGAGCAGAG
CGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGCCGGA
GCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGAC
AAGAATTCCAGCCAAGTCTTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAAGT
AGCCAACCTCACGGAGCCCGTGGTGTCTACTTTCAGCACCAGCTACAGCCGAAGAATGTGA
CTCTGCAATGTGTGTTCTGGGTGAAGACCCACATTGAGCAGCCCGGGGCATTGGAGCAGT
GCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGCAACCACTTGACCTA
CTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGCC
TCCTCTCCTACGTGGGCTGTGTCTCTGCCCCTGGCCTGCCTTGTACCATTGCCGCCTAC
CTCTGCTCCAGGGTGCCCTGCGGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCA
CATGAACCTGCTGCTGGCCGTCTTCTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGG
CCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCCATCTTCTGCACTTCTCCCTGCTC
ACCTGCCTTTCCTGGATGGGCCCTCGAGGGGTACAACCTCTACCGACTCGTGGTGGAGGTCTT
TGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCT
TTCTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACATATGGCCCCATCATCTTGGCTGTG
CATAGGACTCCAGAGGGCGTCATCTACCCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAG
CTACATCACCAACCTGGGCCTCTTACGCCTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCA
CCATGGTGGTGCAGATCCTGCGGCTGCGCCCCACACCCAAAAGTGGTCACATGTGCTGACA
CTGCTGGGCCTCAGCCTGGTCTTGGCCTGCCCTGGGCCTTGATCTTCTTCTCCTTTGCTTC
TGGCACCTTCCAGCTTGTCTGCTCTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCC
TCATCTTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCCTCCCTCTGAAG
AGCAACTCAGACAGCGCCAGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTA
GGCCTCCAGCCCACCTGCCCATGTGATGAAGCAGAGATGCGGCCTCGTCGCACACTGCCTGT
GGCCCCCGAGCCAGGCCAGCCCCAGGCCAGTCAGCCGCAGACTTTGGAAAGCCCAACGACC
ATGGAGAGATGGGCCGTGGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTGGCCTT
GGGGACTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTA
GGGTACTGTCCCCACATCTGTCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTG
GGCCAGCCCTCATTGCTGGGGGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATC
CTGTGCCCCCTGCCTGGGACAGAAATGTGGCTCCAGTTGCTCTGTCTCTCGTGGTCACCCTGA
GGGCACTCTGCATCCTCTGTCAATTTAACTCAGGTGGCACCCAGGGCGAATGGGGCCAGG
GCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTGGCAGGAGCACAGCAGCAG
CTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCCCCCAGTCTCCTCCATCTT
CCCTGGGGTTCTCCTCCTCTCCCAGGGCCTCCTTGCTCCTTCGTTACAGCTGGGGGTCCCC
GATTCCAATGCTGTTTTTTGGGGAGTGGTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGT
TTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCAGGCTCGGTACCGATGCGTGGGCTGG
GCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTGCTCACCTTGACC
AAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAAGTGTGG
ACCATGCCAGTCCCGTCTGGTTTCCATCCCACTCCCAAGGACTGAGACTGACCTCCTCTG
GTGACACTGGCCTAGAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAATAGCTC

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FIGURE 203B

CAGGCGCCCTCGGCCGCCCATCATGGTTAATTCTGTCCAACAAACACACACGGGTTAGATTGC
TGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTGGTCACTCCTCCTGCCAACATTC
AGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAACTCCTGGAGCTACAGGGACAGGGAGCCAT
CATTCCTGCCTGGGAATCCTGGAAGACTTCCTGCAGGAGTCAGCGTTCAATCTTGACCTTGA
AGATGGGAAGGATGTTCTTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAAAAGAAGTA
CATGTTTCATTGTAGAGAATTTGGAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAATCAG
CTGTTGTAATCGCCTAGCAA
AAA

FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRD FLLSDKASSLLCFQH
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTHSFHSPPHATAAHNASVDMCELKRDQLL
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKQVANLTPVVLTFQHQLQPKNVTLCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVSAALACLVTIAAYLCSRVPPLPC
RRKPRDYTIKVHMNLLLAVFLLDTSFLLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE
GYNLYRLVVEVFQTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFSLVFLFNMA MLATMVVQILRLRPHTQKWSHVLTLGLSLVLG
LPWALIFFSFASGTFQLVVLYLFSIITSFQGF LIFIWYWSMRLQARGGPSPLKSN SDSARLP
ISSGSTSSSRI

Important features:**Signal peptide:**

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

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FIGURE 205

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTTCTGTTCAACATGG

FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTCAGGTCCA
GGTTTTGCTTTGATCCTTTTCAAAAACCTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTT
GGATGGGATTATGTGGAACTACCCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCC
ACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGACTCGGGAGTCGCTGCTTCCAAAGT
GCCCCGCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGCT
GACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAAT
TCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATT
ACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAAGAAATAC
GGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACCTTACGTTTGATG
AAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAG
GAACCCAGTGATGGAACATATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAAACA
GATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAAC
CAGGGTTCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCTTCA
GTGCTACCCCTTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTAC
CTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTAT
ATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGGAAGAAAATCCAGAGTGGTG
GATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGT
GTCCATAAGGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTA
AACGCTGTGGTGGGAACCTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCA
AGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGG
ATTGCACAAATCACTACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCA
GAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCACTGC
AGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTT
CAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATT
AGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATC
GTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTA
CGTATTCCACTAGCTGGGTTCTGTATTTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGT
ACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCC
ATGTCCTGGGCCTAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTGCTCATATTCAC
ATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAGGAACATATGTTGCT
ATGAATTAACTTGTGTGCTGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAT
TTCTGCCATTTAGAAGAAGAGAACTACATTCATGGTTTGGGAAGAGATAAACCTGAAAGAAG
AGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTAT
ATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCTATTTTAC
CAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTCAGTTGGTAAATT
TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGAC
AAAAATACATGTATTTTCACTCTCGTATGGTGTGCTAGAGTTAGATTAATCTGCATTTTAAAAA
CTGAATTGGAATAGAATTGGTAAGTTGCAAAGACTTTTTGAAAATAATTAAATTATCATATC
TTCCATTCTGTATTGAGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATTGAGATCC
AGCCATTACTAACCTATTCCTTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACATAAAGC
ACCTTGAAAAGAGACTTGGCAGCTTCCGTATAAAGCGTGCTGTGCTGTGCAGTAGGAACACAT
CCTATTATTGTGATGTTGTGGTTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAAT
ACATGGATATTTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCA
ATTTAAAGAAAATCAGTAAAATATTTTGCTTGTAAAATGCTTAATATNGTGCCTAGGTTAT
GTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAATAAAAGAATGTGGCTATTTTG
GGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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FIGURE 207

MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPKGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY
SCTPRNFSVSI REELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ
LRPKTGVRGLHKSLTDVALEHHEECDVCVRGSTGG

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FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATT
CCATTTTGGGAAGAAGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCTTA
TCCTTTTAAACATAATCCTAATTTCCAAACTCCTTGGGGCTAGATGGTTTCTTAAACTCTG
CCCTGTGATGTCACTCTGGATGTTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCA
TTTGACAGAAATTCCTGGAGGTATTCCCACGAACACCACGAACCTCACCTCACCATTAACC
ACATACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTT
AGATGCAACTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCA
GATTAAACCCAGAAGCTTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACC
AGCTACTAGAGATACCGCAGGGCCTCCCGCCTAGCTTACAGCTTCTCAGCCTTGAGGCCAAC
AACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCAACATAGAAATACTCTACCT
GGGCCAAAACCTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAAGATGCCT
TCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCCT
ACTGTTTTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCA
AGAAGATGATTTTAATAACCTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGCCCTC
GTTGTTATAATGCCCCATTTCTTGTGCGCGTGTAAAAATAATTCTCCCTACAGATCCCT
GTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTTACGTCTACACAGTAACTCTCTTCA
GCATGTGCCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACTGGATCTGTCCCAA
ACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAA
TTGGATCTGTCTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGC
ATTTTCTTCACTGAAAAGCCTGAAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGA
AAAGCTTTAACCTCTCGCCATTACATAATCTTCAAAATCTTGAAGTTCTTGATCTTGGCACT
AACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGACTGAAAGTCATAGA
TCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAATG
CCAGAACTTCTGTAGAAAGTTATGAACCCCAGGTCCTGGAACAATTACATTATTTTCAGATAT
GATAAGTATGCAAGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGA
AAGCTGCTACAAGTATGGGCAGACCTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGT
CCTCTGATTTTTCAGCATCTTTCTTTCCTCAAATGCCTGAATCTGTGAGGAAATCTCATTAGC
CAAACCTCTTAATGGCAGTGAATTTCAACCTTTAGCAGAGCTGAGATATTTGGACTTCTCCAA
CAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGG
ATATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAACTTTACC
AAGAACCTAAAGGTTCTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAG
CAGGACCATGGAGAGTGAGTCTCTTAGAACTCTGGAATTCAGAGGAAATCACTTAGATGTTT
TATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAGAATCTGCTAAAATTAGAGGAA
TTAGACATCTCTAAAATTCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGTATGCCTCC
AAATCTAAAGAATCTCTCTTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCC
AGTGCTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAG
AGATTATCCAACCTGTTCCAGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAG
TCTGACGAAGTATTTTCTACAAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATA
AAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTCAACAATCTGAAGATGTTG
CTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTTGTCTGGTGGGTAA
CCATACGGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCAC
ACAAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG
ATTCTGTTCTCACTTTCCATATCTGTATCTCTCTTCTCATGGTGATGATGACAGCAAGTCA
CCTCTATTTCTGGGATGTGTGGTATATTTACCATTTCTGTAAGGCCAAGATAAAGGGGTATC
AGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTATGACACTAAAGACCCA
GCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAACA
TTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTT
CCCAGAGCATAAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACT
GAAAATTTTAAGATAGCATTTTACTTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGT
GATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAGTCCAAGTTCCCTCCAGCTCCGGAAAA
GGCTCTGTGGGAGTTCTGTCTTGAGTGGCCAACAACCCGCAAGCTCACCCATACTTCTGG
CAGTGTCTAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGA
AACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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FIGURE 209

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG
IPTNTTNTLTLTINHIPDISPASFHRLDHLVEIDFRNCNCPVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR
NPCYVSYSIEKDAFLNLTKLKVLSLKDNVTA VPTVLPSTLTELYLYNNMIAKIQEDDFNNL
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPFRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL
KILRIRGYVFKELKSFNLSPLHNLQNLVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO
TDLDSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLOKLMMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNLSLFLPSGVFDGMPPNLKNLSL
AKNGLKSFWSKKLQCLKNLETLDLSHNQLTTVPERLSNCSRLKNLILKNNQIRSLTKYFLO
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDVWVFWVWNHTEVTIP
YLATDVTVCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAELVAKLEDPREKHFNLCLEE
RDWLPGQPVLNLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

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FIGURE 210A

GGGTACCATTTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACAACAGAAACATGGAA
AACATGTTTCCTTCAGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGTTCCTGTGA
GTTATGCGCCGAAGAAAATTTTTCTAGAAGCTATCCTTGTGATGAGAAAAAGCAAATGACT
CAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAGTTCCCCAAACGGTGGGCAAATAT
GTGACAGAACTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAATCATTTCAAGG
GCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAA
ATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCTCAACCTAAAAAAC
CTAAGGGAGTTACTGCTTGAAGACAACCAGTTACCCCAATACCCTCTGGTTTGCCAGAGTC
TTTGACAGAACTTAGTCTAATTCAAACAATATATACAACATAACTAAAGAGGGGCATTTCAA
GACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAGTCTATTTTAAACAAAGTTTGCGAG
AAAACATAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTATCACTATC
TTTCAATTCTCTTTCACACGTGCCACCCAAACTGCCAAGCTCCCTACGCAAACCTTTTTCTGA
GCAACACCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTA
CTAGATTTAAGCGGGAAGTGTCCGAGGTGCTTCAATGCCCCATTTCCATGCGTGCCCTGTGA
TGGTGGTGCTTCAATTAATATAGATCGTTTTGCTTTTCAAACCTTGACCCAACTTCGATACC
TAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGTTTAAAAATATGCCTCAT
CTGAAGGTGCTGGATCTTGAATTCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCATTTTT
AACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATC
CACAGCATATTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCATTTA
AGAGGTTATGTGTTCCAGGAAGTCAAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAA
CTTATCGACTATCAACTTGGGTATTAATTTTATTAAGCAAATCGATTTCAAACCTTTTCCAAA
ATTTCTCCAATCTGGAAATTATTTACTTGTGAGAAACAGAAATATCACCGTTGGTAAAAGAT
ACCCGGCAGAGTTATGCAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAAC
AGATTTTGAGTTTGACCCACATTCGAACCTTTTATCATTTACCCGTCCTTTAATAAAGCCAC
AATGTGCTGCTTATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCA
AACCAATTTGAAAATCTTCTGACATTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCA
AGTGTTAAGTGGAAGTGAATTTTCAGCCATTCCTCATGTCAAATATTTGGATTTGACAAACA
ATAGACTAGACTTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGGAAGTTCTAGAT
CTCAGCTATAATTCACACTATTTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATTCA
AAATTTACAAATCTAAAAGTTTTAACTTGAGCCACAACAACATTTTATACTTTAACAGATA
AGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTTCAGTGGCAATCGCCTTGACATT
TTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAATCTGACACG
TCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCTTAAATTTGCCAG
CGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAACTGGACATTACTC
CAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGA
TAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCC
ACCTACCTCTGGCTTTCTTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAAT
CTGCTAAAAACAATCAACAAATCCGCACTTGAACTAAGACCACCACCAAATTATCTATGTT
GGAAGTACACGGAAACCCCTTTGAATGCACCTGTGACATTGGAGATTTCCGAAGATGGATGG
ATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCATTTGTGCCAGTCTGGGGAT
CAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAGATGTCACTGCAGT
GATATTATTTTCTTCACGTTCTTTATCACCAACATGGTTATGTTGGCTGCCCTGGCTCACC
ATTTGTTTTACTGGGATGTTTGGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTAC
AGGTCTCTTTCCACATCCCAAACCTTTCTATGATGCTTACATTTCTTATGACACCAAAGATGC
CTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAGAGAGCCGAGACAAAA
ACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACCTC
ATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAG
CTGGAACCTTTAAAACAGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATG
TGATTATATTTATCCTGCTGGAGCCAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAG
CGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTG
GCAAACCTCTGAGAAATGTGGTCTTGACTGAAAATGATTCACGGTATAACAATATGTATGTCG
ATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTGCGCCATAATAAAGATGCAAA
GGAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATATCCCAAACCTTAGTGG
TTTAAACAACACATTTGCTGGCCACAGTTTTTGAGGGTCAGGAGTCCAGGCCCAGCATAA

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FIGURE 210B

CTGGGTCCTCTGCTCAGGGTGTCTCAGAGGCTGCAATGTAGGTGTTACCAGAGACATAGGC
ATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCA
AAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCCACAAGGCAGCTTGCTTCATCAGAGCT
AGCAAAAAGAGAGGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAG
TGATATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAGCT
CCATGGGAGTGACCACCTCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTCTGAT
TGCTTCAGTTGGTCATCAACTATTTCCCTTGACTGCTGTCCTGGGATGGCCTGCTATCTTG
ATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACCATCTTAGCAGTTGACCTAA
CACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATATTAAGC
TGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTGC
GTTTTATTTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATG
CCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAA
GTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGCCATTGCTGTAAATCTTAA
AATGAATGAATAAAAATGTTTCATTTTACAAAAA

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSPCDEKKQND SVIAECSNRRLQEVPTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTEL SLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNL TQLRYLNLSSSTSLRKINA AWFKNM
PHLKVLDLEFN YLVGEIVSGAFLTMLPRLEILDLSFN YIKGSYPQHINISRNF SKLLSLRAL
HLRGYVFQELREDDFQPLMQLPNLSTINLGINF IKQIDFKLFQNF SNLEIIYLS ENRISPLV
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELS DLEV
LDLSYN SHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYT LT DKYNLESKSLVELVFSGNRL
DILWNDDDNRYISIFKGLKNLTRLDSLNLRLKHIPNEAFLNLPASLTE LHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTL LLSHNRISHLPSGFLSEVSSLKHLDLS
SNLLKTINKSALETKTTTKLSMLELHG NPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRGKSIVSLELTTCVSDVTAVILFFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK
GYRSLSTSQT FYDAYISYDTKDASVTDWV INELRYHLEESRDKNVLLCLEERDWD PGLAIID
NMQSINQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDV IIFILLEPVLQHSQYLRL
RQRICKSSILQWPDNPKAEGLFWQTLRNVVL TENDSRYNMYVDSIKQY

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FIGURE 212

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCGTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT
CTGGTGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTCCTG
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA
AAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

FIGURE 213

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSadgtLCVpKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDpGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

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FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCAGCTTGGCTGGGCCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCCAACGGGGGCCCCGGGGAGGGGAAGTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCCG
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCATCCTTCCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCTTCTTCTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGA
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCCTCCTCTTCTCCTCCCTTCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC
CCCCAGCACATAAAAATGAAACGTG

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FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSadgtLCVpKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

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FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCCTCC
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCTTCCTCGGGAG
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTG

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FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

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FIGURE 218

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCTTGTCAGGAGGAGACAGCCTC
CCGGCCCCGGGGAGGACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTC
CGTTTCCTGCCGTACAGCTGCCGGCCGAGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTC
CTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGGAGATTGTCTTCCAGGGCTAGCAA
TTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGATTTCAAAGCTG
GGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAAACCCATTTTGGAGCAGGAATTCCAA
TCATGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCCAGGCAGG
AACACCTTTTGCTGTGATGGCCGCGTCATGATGGCCCGGCCAAAAGGGCATTTTCTACCTGAC
CCTTTTCCTCATCCTGGGGACATGTACACTCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTG
TTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCTTCCTTTTCTCCATGGCTACA
CTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATGAAGCAGC
TTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGC
CTCGTATCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGC
AAGATCTTCCGGCCTCCCCGGGCCTCCCATTGCAGCATCTGTGACAACCTGTGTGGAGCGCTT
CGACCATCACTGCCCCCTGGGTGGGGGAATTGTGTTGGAAAGAGGAACTACCGCTACTTCTACC
TCTTCATCCTTTCTCTCTCCCTCCTCACAACTCTATGTCTTCGCCTTCAACATCGTCTATGTG
GCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAAACTCCTGGAACCTGTTCT
AGAAGTCCTCATTTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCTACTT
TCCTCGTGGCTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGGAAGAAT
CGCGTCCAGAATCCCTACAGCCATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGG
CCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTATTTTGCCACTGGAGGAAAGTGGAAGTC
GACCTCCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCCCAGCCCCCACAGAA
CACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAGA
GCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACT
TTTGTGTTGTGTTAATTAGGGCTATGAGAGATTTTCAGGTGAGAAGTTAAACCTGAGACAGAG
AGCAAGTAAGCTGTCCCTTTTAACTGTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTG
GCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACTCAAGGCAGTGGCAGAAAGATGTCAG
TCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCTCCATGGCCTCA
GCCACAGGGTCCCCTTGGACCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTC
ACTGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCA
CGTGCTGAGTCCAGAGGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTTGG
GGTCTTCAGGACTGAAGAGGAGGGAGAGTGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCC
AGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCTTCCACTTGTTGTANNNNNNNN
NNNNNNNNNNNNNNNNNNNTTGTTTTTCTTTTGAATCCTGCTCCCATTAGGAGCAGGAATG
GCAGTAATAAAAGTCTGCACTTTGGTCAATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACT
TAAACACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGG
AAACCAAGGCACAGAGAGGCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAA
AAAAATGCTAACCAGTTCTTCCATTAAGCCTCGGCTGAGTGAGGGAAAGCCCAGCACTGCTG
CCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCTATGGTAACCACACTGGGG
GCTTCTTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTTCACCC
TGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTTCAAGGAAGAAG
ATTTATGTATTATATGTGGCTATATTTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAG
GGTCTGTCTGGATGACTTATGCGGTGGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAA
GGCGATTAACTGTGTCTAATGCA

**FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAV.
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGN CVGKRNYRYFYL
FILSLSLLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLI CFFTLWSVVG LTGFHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPPQEAAEAEK

FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCCTTTCT
CCCACAGAGCNCCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA
CAAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATTTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC
GAATACTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCCTCAGCAGAATTCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGCCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTAAAAAAGAAATTGAA
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

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FIGURE 222

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGT LQCEASAV
PSAEFQWYKDDKRLIEGKKG VKVENRPFLSKLIFFNVSEHDY GNYTCVASNKLGHTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLL LKF

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FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

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FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGCCCGGGAGCGGGCCAGCTG
CCGGGAGCCCTGAATCACCGCCTGGCCCGACTCCACCAATGAACGTCGCGCTGCAGGAGCTGG
GAGCTGGCAGCAACGTGGGATTCCAGAAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAG
CTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCTGCACTGCTTCTGGGCTGCCTTGT
GGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACAGAGGCCTGCA
TTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTT
TACCAGTTCTCCTGTGGGGGGCTGGATTCCGAGGAACCCCTGCCCGATGGGCGTTCTCGCTG
GAACACCTTCAACAGCCTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACA
CCACCTTCAACTCCAGCAGTGAAGCTGAGCAGAAGACACAGCGCTTCTACCTATCTTGCCTA
CAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGAGACCTCATTGAGAAGATTGG
TGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAGGCAGTAG
CAGGGACCTACAGGGGCCACCCCATCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCC
AACAGCAATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTT
AAACAGAACTGCCAATGAGAAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACTGGGGA
TGCTGCTGGGTGGGCGGGCCACCTCCACGAGGGAGCAGATGCAGCAGGTGCTGGAGTTGGAG
ATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGGACGAGGAGAAGATCTACCA
CAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTCCTGT
CTTTCTTGCTGTCACCATTTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGAT
TATTTGCAGCAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCT
GATCTGGAACCTGGTGCAAAGACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAG
AGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAGTCCTGTGTGCCGAGGTGGCAGACCTGC
ATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTCGTGAAGGCCACGTT
TGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAGG
AGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCA
GATGCCATCTATGATATGATTGGTTTCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGA
TGTTTATGACGGGTACGAAATTTCTGAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACA
ACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAGCCTCCCAGCCGAGACCAGTGGAGC
ATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATCGTCTTCCCCGC
TGGCATCCTGCAGGCCCCCTTCTATGCCCCGAACCACCCCAAGGCCCTGAACCTCGGTGGCA
TCGGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGAC
AAAGAAGGGAACCTGCGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACAC
GGCCTGCATGGAGGAACAGTACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCC
AGACGCTGGGGGAGAACATTACTGACAACGGGGGGGCTGAAGGCTGCCTACAATGCTTACAAA
GCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTACCAACCACCA
GCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACG
AGGGGCTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAAC
TCCCGTGACTTCCTGCGGCACCTCGGCTGCCCTGTGCGCTCCCCATGAACCCAGGGCAGCT
GTGTGAGGTGTGGTTAGACCTGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCA
GCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGT
CTAGTCCCTCCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCT
CTGCTTTGGGGGTGCCCTGCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGT
GTCACCCTGCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTC CATAGGAAGGAGTCTGCC

FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPF FTVYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVL TAY
LDYMEELGMLLGGRPTSTREQMQQVLELEIQ LANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLLESDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLLETLYGTTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLYNFS AKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLA AFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLP AVGLTNHQLFFVGFAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNP GQLCEVW

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FIGURE 226A

GCCCCGGCCCTCCGCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCGCTCCCGCGCCCTCCTC
CCTCCCTCCTCCCCAGCTGTCCCGTTTCGCGTCATGCCGAGCCTCCCGGCCCGCCGGCCCCG
CTGCTGCTCCTCGGGCTGCTGCTGCTCGGCTCCCGGCCGGCCCGCGGGCGCCGGCCCCAGAGCC
CCCCGTGCTGCCCATCCGTTCTGAGAAGGAGCCGCTGCCCGTTCGGGGAGCGGCAGGTAGGT
GGGCGCCCCGGGGGAGGCGCGGGCGGGGAGTCGGGGCTCGGGGCGAGTCAGCGCCAGCCCCGAG
GGGGCGCGGGGGCGCAGGTGGCTCGGCGCGGGCGGGCGGCCCGGAGGGTGGGCGGGGGCAGAAG
GGCGCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGCGGCACACGGCGCGAGCTG
GGCAGCGGCCTCCAGCCAAGCCCGTCCCCGCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCC
TTGGACGAGACGTGGCACCCGGACCTAGGGGAGCCATTCGGGGTGATGCGCTGCGTGCTGTG
CGCTGCGAGGCGCAGTGGGGTCGCCGTACCAGGGGCCCTGGCAGGGTCAGCTGCAAGAACA
TCAAACCAGAGTGCCCAACCCCGGCCTGTGGGCAGCCGCGCCAGCTGCCGGGACACTGCTGC
CAGACCTGCCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTTCGAGGCGGTGGCACG
AGCCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCCTACAGGCGGCTGGACC
GCCCTACCAGGATCCGCTTCTCAGACTCCAATGGCAGTGTCTGTTTGAGCACCCCTGCAGCC
CCCACCCAAGATGGCCTGGTCTGTGGGGTGTGGCGGGCAGTGCCTCGGTTGTCTCTGCGGCT
CCTTAGGGCAGAACAAGCTGCATGTGGCACTTGTGACACTCACTCACCCCTTCAGGGGAGGTCT
GGGGCCCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGACTCTA
GAAGGCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGA
CTCCTTGCATTTTTTTGTGCTCTTCCGAGGCCCTGCAGGACTAACCCAGGTTCCCTTGAGGC
TCCAGATTCTACACCAGGGGCAGCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAA
CCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGTCCAGGAGATGGACTGGCTGGTGCTGGG
GGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCATCAGTGGACACATTG
CTGCCAGGAAGAGCTGCGACGTCCTGCAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCCA
GTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCCTGATCCT
CCAGGTGCAATTGGTAGGGACAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTC
AGCGGAGGGATCAGCCCACTGTCCTGTGCCACATGGCTGGCCTATCCTCCCCTGCCCCCAGG
CCGTGGGTATCTGCCCTGGGCTGGGGTGGCCGAGGGGCTCATATGCTGCTGCAGAATGAGCT
CTTCTGAACGTGGGCACCAAGGACTTCCCAGACGGAGAGCTTCGGGGGCAACGTGGCTGCC
CTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTA
CCCCCTGTGAAGAGCCAAGCAGCAGGGCACGCCTGGCTTTCTTGGATAACCACTGTACCT
GCACTATGAAGTGCTGCTGGCTGGGCTTGGTGGCTCAGAACAAGGCACTGTCACTGCCACC
TCCTTGGGCCCTCCTGGAACGCCAGGGCCTCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAG
GCCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACCTGCTGCGGCACCTGGCAAAGGCATGGC
TTCCCTGATGATACCAACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCTCTCCTCCC
AGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAG
GGGGTGCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCT
CCCGGCCCTAGCGCCCGCCAAACCTGGTGGTCTGGGCGGCCCCGAGACCCCAACACATGCT
TCTTCGAGGGGCAGCAGCGCCCCACGGGGCTCGCTGGGCGCCCAACTACGACCCGCTCTGC
TCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGTGGTGTGCCACCGCCAG
CTGCCACACCCGGTGCCAGGCTCCCGACCAGTGCTGCCCTGTTTGCCCTGGCTGCTATTTTG
ATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCTTTGGC
TTAATTAAGTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAA
GGTGCAGTGTCCCCGGCTGGCCTGTGCCAGCCTGTGCGTGTCAACCCCAACCGACTGCTGCA
AACAGTGTCCAGGTGAGGCCACCCCAAGCTGGGGGACCCATGCAGGCTGATGGGCCCCCGG
GGCTGCCGTTTTGTGCTGGGCAGTGGTTCCAGAGAGTCAGAGCTGGCACCCCTCAGTGCCCC
GTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGTGT
GAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCAGGGAGGTCCCTGAAGAA
GCTGAAGGTCACTGTGTCCAGTGCCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACC
AGGCAGGGGTGCCTCACTGTGAGCGGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGG
AAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCCAACGGCGGCGTAAGTGAGGGAGTCCAGG
GTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAGGGAAGGGAGCAC
TCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCCCTCACAGC
AACCTGGTGGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGA
AATTAAGCAACGAGATGAAGGTCACCCAGCTGTGTGCACTGACCTGTTTAGAAAATACTGGC

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FIGURE 226B

CTTTCTGGGACCAAGGCAGGGATGCTTTGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCAC
TCCCTCTCCCCTCCTCCAACATTCCCTCCCTTCTGTCTCCAGCAGCCCCAGAGACCAGAACT
GATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCCAAGTGACCA
AGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCAATTCTCCTGTGG
GAAGCCCAGTGCCTTTGCTCCTCTGTCCTGCCTCTACTCCCACCCCCACTACCTCTGGGAAC
CACAGCTCCACAAGGGGGAGAGGCAGCTGGGCCAGACCGAGGTCACAGCCACTCCAAGTCCT
GCCCTGCCACCCTCGGCCTCTGTCTGGAAGCCCCACCCCTTTCTTCCTGTACATAATGTCA
CTGGCTTGTTGGGATTTTTAATTTATCTTCACTCAGCACCAAGGGCCCCGGACACTCCACTC
CTGCTGCCCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTGTATTTATTAAACATTTCT
TTTTTCAGTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGG
AGAAGGGGCGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGA
CCTGGAGAGGCAGAGGATAGCGTGGC NNTTGGCTGGCATNCCTGGGTTCGCGAGAGGGGCTG
GGGATGGTTCTTGAGATGGTCTAGAGACTCAAGAATTTAGGGAAGTAGAAGCAGGATTTTGA
CTCAAGTTTAGTTTCCCACATCGCTGGCCTGTTTGCTGACTTCATGTTTGAAGTTGCTCCAG
AGAGAGAATCAAAGGTGTCACCAGCCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCTTTC
CCTCCCCTCCCCTCCCCTCCCCTCCCCTCC

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FIGURE 227

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCGCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTGGA
GGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAAACTGCCCT
CCTTTCTTTCTTCTTTTCTTCTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCTCCTTCC
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTCATGGACCT
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

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FIGURE 228

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT
TTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCCACA
GGTGACATGAGTACAGACCCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTCACCCTGCCTGGAAGAG
GTCTGGGTGGGGAGGCCAGTTC CATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTTTCCCTGGGCTGAGAGGGGAAGTG CATATGTGTAGCGGGTACTGGTTCCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT
TGGCCCTTATAGGACC